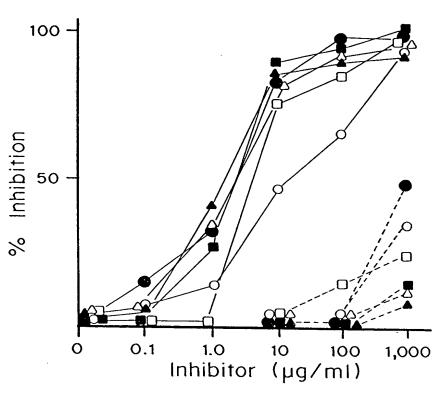
Continuation of U.S.S.N. 08/800, 682 OMRF 150C 'CON





F/G. 1

Continuation of U.S.S. N. 08/800, 682 OMR - 58 -P CON

FIG. 2a

GGT GAA GAA GGA GTT GTG CCA GCA CGT GAG TAC TCA GAC GAT CGT 45 Gly Glu Gly Val Val Pro Ala Arg G lu Tyr Ser Asp Asp Arg [15]

AAC ATC AAC CTG GCA GAC GAA TTA AAA ATT GGT GAT ACC ATT GAA 90 Asn Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu [30]

GCA GTT GTC ATT TCT AAC GTA ACA AGC GAC AAG GAA GGC GTC AGT 135 Ala Val Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser [45]

TAC TTG TTG TCA AAG AAG CGT TTG GAT GCG CGC AAG GCA TGG GAA 180 Tyr Leu Leu Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu [60]

AAC TTG AGC TTT GCT GAA GGT GAC ACAGTT GAT GCC AAG GTT ATC 225 Asn Leu Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile [75]

AAC GCT GTT CGT GGT GGT TTG ATT GTT GAT GTT AAC GGC GTA CGT 270 Asn Ala Val Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg [90]

GGT TTC GTA CCA GCA TCA ATG GTT GCA GAA CGT TTC GTT TCT GAT 315 Gly Phe Val Pro Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp [105]

TTG_AAC CAA TTC AAG AAT AAG GAT ATT AAA GCA CAA GTT ATC GAA 360 Leu Asn Gin Phe Lys Asn Lys Asp IIe Lys Ala Gin Valile Glu [120]

ATT GAC CCT GCT AAT GCA CGT TTG ATT TTG TCA CGT AAG GCT GTT 405 Ile Asp Pro Ala Asn Ala Arg Leu Ile Leu Ser Arg Lys Ala Val [135]

GCT GCA CAA GAA CGC GCT GCA CGA TTG GCT GAA GTA TTT AGC AAG 450 Ala Ala Gln Glu Arg Ala Ala Gln Leu Ala Glu Val Phe Ser Lys [150]

TTG TCA GTT CGT GAA GTT GTT GAA GGA ACT GTT GCC CGT TTG ACA 495 Leu Ser Val Gly Glu Val Val Glu Gly Thr Val Ala Arg Leu Thr [165]

GAC TTC GGC GCA TTC GTT GAC TTG GGT GGT GGT GGT GGT TTG GTT 540 Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu Val [180]

CAC GTA TCA GAA ATC TCA CAC GAT CGT GTG AAG AAC CCG GCC GAT 585 His Val Ser Glu I le Ser His Asp Arg Val Lys Asn Pro Ala Asp [195]

GTA TTG ACA AAG GGT GAC AAG GTT GAT GTT AAG ATC TTG GCA TTG 630 Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys IIe Leu Ala Leu [210]

GAC ACT GAA AAG GGT CGT ATC TCA TTG TCA ATC AAA GCA ACA CAA 675 Asp Thr Glu Lys Gly Arg IIe Ser Leu Ser IIe Lys Ala Thr Gln [225]

Continuation of 4.5.5. N. 08/800, 682 OMRAYSS EP CON

FIG. 2b

						_	<i>,</i> σ .								
CGT A rg	GGA G ly	CCT P ro	TGG T rp	GAC A sp	GAA G Iu	GCT A la	GCA A la	GAT A sp	CAA G In	ATC Ile	GCT A la	GCA Ala	GGT GIV	TCA S er	720 [240]
GTG	СТТ	GAA	GGT	ACT	GTT	AAG	CGT	GTG	AAG	GAC	П	GGT	GCC	П	
GTT	GAA	АТТ	TTG	CCT	GGT	ATC	GAA	GGT	СТТ	GTG	CAC	GTG	TCA	CAA	
ATT	TCA	AAC	AAG	CGT	ATT	GAA	AAC	CCA	TCA	GAA	GTT	TTG	AAG	TCT	_
GGT	GAC	AAG	GTA	CAA	GTG	AAG	GTA	TTG	GAC	: ATT	AAG	CCA	GCC	GAA	900
GAA	CGT	ATT	TCA	TTG	TCA	ATG	AAG	GCT	TTG	GAA G lu	GAA	AAG	CCA	GAA	945
CGT	GAA	GAT	CGT	CGT	GGT	AAC	GAT	GGT	TCA	GCT A la	TCA	CGT	GCT	GAT	990
ATC	GCT	GCT	TAC	AAG	CAA	CAA	GAT	GAC	TCA	GCC A la	GCA	ACA	TTG	GGT	1035
GAC	ATC	Ш	GGT	GAT		TTG	TAA			CAAC				-	
GCC	AGTT	стт	ΤΑΤΤ	TTGA	AGAA	AAAT	TGAGT	rggg	CATTA	AGTGG	GCG	CTCAG	CGGTA	AŢĢ.	1145
AAA	AAGG	AGGT	GCGA	TATTA	GGCA	GCAC	CAGT	AGTA	GCCA	TTGTT	GGC	GACC	AAAC	GTCG	1204
GAA	AATC	GACT	ATCT	TTAA	CCGG	ATGG	CCGG	AGAA	CGTA ⁻	TTGCA	WITE	STTGA	AGAT	CÁA	1263
CCA	GGG)AATE	CACG	CGAT	CGTTT	GTAC	GCGC	CAG(CCGA	ATGGT	TGAA	TATT			1314

Continuation of U.S.S.N. 08/800, 682 OMRITISSEP CON

F/G. 33

HS1	1 63 SFAEGDTVDAKVINAVRGGLIVDVNGVRGFVRASINIVARERHVSDLNQFKNKDIKAQVIEI 121	
ES1	1 101 AYEDAETGVINGK-K FT-ELD - I - A-L- G- L -\QV-IP-IR -TLHLEG-ELEFK KL 159	_
RS1	RS1 107 K- EA- ER- EGI IF- Q-KFTLD -AVA/-L- RIQ - DI PIR -VTPADAQPAALRNLKM 165	
PS	1 1 ETGVINGK-KFT- EL1 - A - L- G L - D V-P -R-TTHLEG -ELEFK KL 54	
CS ₁	1 182 DVV-KG- IVG-NKVVAL-E -L FIQII SBK SAEELLE - E-PLKFV - V 236	
•	0 q & B & B & B & B & B & B & B & B & B &	

L 113 INL 287	, c.
55 -QKRNNVVVRIES - SS- ERDQLLEN -QE-ME-K- I -KN Y L 113 237 -EEQSVM-NRKAM-DSQ- M- DSQAQ-GI- S T QS-KPY I - I I N L 287 d e ****	HS1 122 DPANARLILSRKAVAAUERAAULAEVFSKLSVGEVVEGIVAKLIUFGAFVDLGGVDGLV 180 ES1 160 -QKRNNVVVRIES - NS- ERDOLLEN-QE- ME-K-I-KNY
-IES - SS- ERDQLLI AM-DSQ- M- DSQ d ****	VAAUERAAULAEVR -IES - NS- ERDQLL -LEESE - RS-IVC
55 -QKRNNVVR- 237 -EEQSVM-NRK ***	122 DPANARLILSKKAV 160 -QKRNNVVVR 166 -KRRGNIVVRT
CS1	HS1 ES1

239	277	283	172	,337		
KGRISLSIKATQRGPWDEAADQIAAG	FS1 219 -ITDMAWKH-SEIVNV E ITV-KF-R- RT -VGL-QLGEDVAI - KRYPE- 27	FH GM-QLESDGIGAKYPV-	RT -VGL-QLGEDVAI - KRYPE-	288 Q SDI - T QP TLK - MSH-R- R V T-KLEPT - G-	ס	***
GDKVDVKILALDTE	E IT V-KF-R- F	- QQ-K- Q- IRINQ- T	E IT V-KF-R- F	TLK - MSH-R- F	O	****
RVKNPADVLTK	(H-SEIVNV	AH-SEIQNI	H-SEIVNV	SDI-T0P-	q	
181 HVSEISHDI	219 -ITDMAWK	225 TDMAWI	114 -ITDMAWK	288 0	G	***
HS.1	7. S.	12.	Z 2	SS		

Continuation of U.S.S.N. 08/800,682. OMRF 158 TPCON

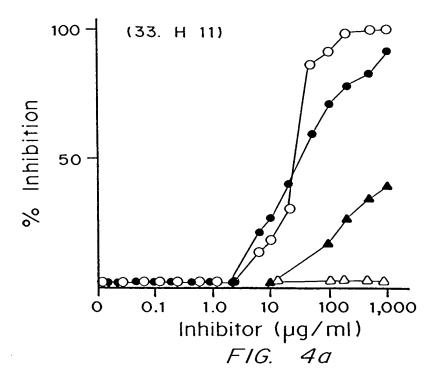
FIG. 3b

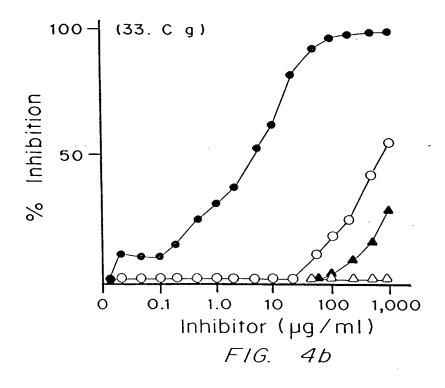
		V 430		•	
NKRIENPSEVLKSGDKVQVKVLDIKI	I RD-V-DATLSV E- EA- FTGVC	-RPG-QVI-EFNKV- RAVVD	1 K E IAAV QVDA		
HS1 240 SVLEGTVKRVKDFGAFVEILPGIEGLVHVSQISNKRIENPSEVLKSGDKVQVKVLDIKP	278 TK -T -R- TNLT -Y- CEE -V EM RD-V-DATLSV E- EA- FTGVDR	RS1 284 KKIS TNIT -Y LE I - I - EM -RPG-QVI-EFNK V - RAV VDV	173 TK-T -R - TNLT -Y- CEE -V EN	٥	****
HS1	ES1	RST	PS		

299 AEERISLSMKALEEKPERE 317 511 KNRA----VR-KD-AD-KD 529 431 DK -----GI-QL 320 ER -----GV-QLA-DP 335

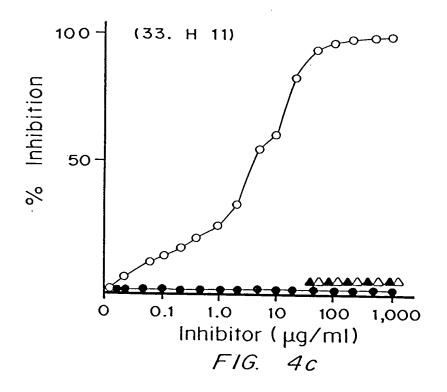
HST FST PST

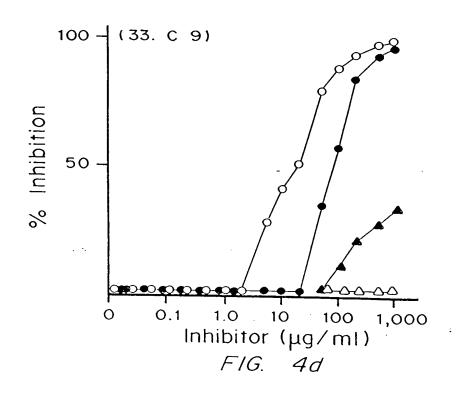
Continuation of U.S.S.D. 08/800, 682 OMRF 1500 CON





Continue of 4.55 N. 08/800,682





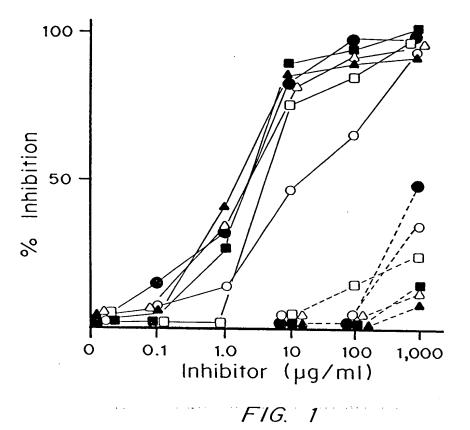


FIG. Za

E16.-2

GGT GAA GAA GGA GTT GTG CCA GCA CGT GAG TAC TCA GAC GAT CGT 45 Gly Glu Gly Val Val Pro Ala Arg G lu Tyr Ser Asp Asp Arg [15]

AAC ATC AAC CTG GCA GAC GAA TTA AAA ATT GGT GAT ACC ATT GAA 90 Asn Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu [30]

GCA GTT GTC ATT TCT AAC GTA ACA AGC GAC AAG GAA GGC GTC AGT 135 Ala ValValle SerAsn ValThrSerAsp LysGluGly ValSer [45]

TAC TTG TTG TCA AAG AAG CGT TTG GAT GCG CGC AAG GCA TGG GAA 180 Tyr Leu Leu Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu [60]

AAC TTG AGC TTT GCT GAA GGT GAC ACAGTT GAT GCC AAG GTT ATC 225 Asn Leu Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile [75]

AAC GCT GTT CGT GGT GGT TTG ATT GTT GAT GTT AAC GGC GTA CGT 270 Asn Ala Val Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg [90]

GGT TTC GTA CCA GCA TCA ATG GTT GCA GAA CGT TTC GTT TCT GAT 315 Gly Phe Val Pro Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp [105]

TTG AAC CAA TTC AAG AAT AAG GAT ATT AAA GCA CAA GTT ATC GAA 360 Leu Asn Gin Phe Lys Asn Lys Asp IIe Lys Ala Gin Valile Glu [120]

ATT GAC CCT GCT AAT GCA CGT TTG ATT TTG TCA CGT AAG GCT GTT 405 Ile Asp Pro Ala Asn Ala Arg Leu Ile Leu Ser Arg Lys Ala Val [135]

GCT GCA CAA GAA CGC GCT GCA CGA TTG GCT GAA GTA TTT AGC AAG 450 Ala Ala Gln Glu Arg Ala Ala Gln Leu Ala Glu Val Phe Ser Lys [150]

TTG TCA GTT CGT GAA GTT GTT GAA GGA ACT GTT GCC CGT TTG ACA 495 Leu Ser Val Gly Glu Val Val Gly Gly Thr Val Ala Arg Leu Thr [165]

GAC TTC GGC GCA TTC GTT GAC TTG GGT GGT GGT GGT GGT TTG GTT 540 Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu Val [180]

CAC GTA TCA GAA ATC TCA CAC GAT CGT GTG AAG AAC CCG GCC GAT 585 His Val Ser Glu I le Ser His Asp Arg Val Lys Asn Pro Ala Asp [195]

GTA TTG ACA AAG GGT GAC AAG GTT GAT GTT AAG ATC TTG GCA TTG 630 Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu Ala Leu [210]

GAC ACT GAA AAG GGT CGT ATC TCA TTG TCA ATC AAA GCA ACA CAA 675 Asp Thr Glu Lys Gly Arg Ite Ser Leu Ser Ite Lys Ala Thr Gln [225]

FIG. 26

						_	— , —,		~						
CGT A ro	GGA G Iv	CCT P ro	TGG T m	GAC A sp	GAA G Iu	GCT A la	GCA A la	GAT	CAA	ATC	GCT	GCA	GGT	TCA	720 [240]
3	,			тор		,u	71 lu	Λοp	u III	110	Λ Ια	Міа	ч	3 EI	[240]
GTG V al	CTT L eu	GAA G I u	GGT G ly	ACT T hr	GTT V al	AAG Lys	CGT A rg	GTG V al	AAG Lys	GAC A sp	TTT Phe	GGT G I y	GCC Ala	TTT Phe	765 [255]
GTT V al	GAA G Iu	ATT Ile	TTG L eu	P to	GGT G I y	ATC Ile	GAA G lu	GGT G ly	CTT L eu	GTG V al	CAC His	GTG V al	TCA S er	CAA G In	810 [270]
ATT I le	TCA S er	AAC A sn	AAG Lys	CGT A rg	ATT I le	GAA G I u	AAC A sn	CCA Pro	TCA S er	GAA G lu	GTT Val	TTG L eu	AAG L ys	TCT S er	855 [285]
GGT G ly	GAC A sp	AAG L ys	GTA V al	CAA G In	GTG V al	AAG Lys	GTA V al	TTG L eu	GAC A sp	ATT I le	AAG L ys	CCA P ro	GCC A la	GAA G Iu	900
GAA G lu	CGT A rg	ATT I le	TCA S er	TTG L eu	TCA S er	ATG M et	AAG L ys	GCT A la	TTG L eu	GAA G Iu	GAA G lu	AAG L ys	CCA P ro	GAA G lu	945 [315]
CGT A rg	GAA G lu	GAT A sp	CGT A rg	CGT A rg	GGT G ly	AAC A sn	GAT A sp	GGT G ly	TCA S er	GCT A la	TCA S er	CGT A rg	GCT A la	GAT A sp	990 [330]
ATC I le	GCT A la	GCT A la	TAC T yr	AAG L ys	CAA G In	CAA G In	GAT A sp	GAC A sp	TCA S er	GCC A la	GCA A la	ACA Thr	TTG L eu	GGT G ly	1035 [345]
GAC A sp	ATC I i e	TTT P he	GGT G ly	GAT A sp	AAG Lys	TTG L eu	TAA ***	GAG	GCAT	CAAC	ATAA	AAGA	GCTG	GTTC	1086 [352]
GCC	AGTT	стт	TTTA	TTGA	AGAA	AAAT	rgagt	GGGG	CATTA	GTGG	GCG	CTCAC	ÇGGTA	ιŢĢ	1145
AAA	4AGG.	AGGT	GCGA	TATT	GGCA	GCAC	CAGT	AGTA	GCCA	TTGTT	GGC	GACC	4AAC(STCG	1204
GAA	AATC	GACT	ATCT	TTAA(CCGGA	ATGG	CCGG	AGAA	CGTAT	TTGCA	ATTG	ITTGA	AGAT	CAA	1263
CCA	GGGG	STAAC	ACG(CGAT(CGTTT	GTAC	GCGC	CAGO	CCGAA	ATGGT	TGAA	TATT			121/

FIG. 3a

	* * * *	****	****	* * *	
	Q	C	Ω	C	!
337	VT-KLEPT-G-	- TLK - MSH-R- R	SDI-TQP-	288 0	5.53
283	H GM-QLESDGIGAKYPV- T -VGL-OLGEDVAI - KRYPE-	. QQ-K- Q- IRINQ- TI - F IT V-KF-R- R	// WR H-SEIQNI - // K H-SFIVNV-	225TDMAV	RS1
277	181 HYSEISHURVKNPADVLIRGDRYDVKILALDIENGRISLSINATUNGFYNDEAGUMAG 219 -ITDMAWKH-SEIVNV E ITV-KF-R- RT -VGL-QLGEDVAI - KRYPE-	3DKVDVKILALDI EN E ITV-KF-R- R	DRVKNPADVLI K VKH-SEIVNV	181 HVSEISH 219 -ITDMAW	13. 13. 13.
•	* * * * * * * * * * * * * * * * * * *	***		* *	
287	237 -EEQSVM-NRKAM-DSQ- M-DSQAQ-GI-STQS-KPYI-IINL	M- DS0AQ-61- S	/WN ILS - SS /M-NRKAM-DSQ-	237 -EEQSV	
224	166 -KRRGNIVVRT -LEESE - RS-IVQN -EE-'QV-KNIY 1 L 224	E - RS-IVQN -EE- Q-	WRT -LEES	166 -KRRGNIN	RS1
218	160 -QKRNNVVVRIES - NS- ERDQLLEN-QE- ME-K- I -KNY 218	- ERDQLLEN-QE- M	WRIES - NS	160 -QKRNNV	ES1
180	122 DPANARLILSRKAVAAQERAAQLAEVFSKLSVGEVVEGTVARLTDFGAFVDLGGVDGLV 180	AQLAEVFSKLSVGEN	ILSRKAVAAQERA	122 DPANARL	HS1
	a b ****				
98	182 DVV-KG-IVG-NKVVAL-E -L F-Q I SSK -SAEELLE - E-PLKFV - V 236	AL-E-L F-Q	-KG- IVG-NKVV	182DW-	
54	ETGVINGK-KFT- ELI - A - L- G-L - DV-P-R-TTHLEG -ELEFK KL 54	- EL1-A-L-G-L	-TGVINGK-KFT	Т	
65	107 K- EA- ER- EGI IF- Q-KFTLD -AVA -L- R-Q - DI -PIR -VTPADAQPAALRNLKM 165	LD-AVA-L-R-Q	- EGI IF- Q-KFI	107 K- EA- ER-	RS1
29	101 AYEDAETGVINGK-K FT-ELD - I - A-L- G- L- DV-P-R -TLHLEG-ELEFK KL 159	T-ELD - I - A-L- G- L	-TGVINGK-K F		ES1
7	63 SFAEGDTVDAKVINAVRGGLIVDVNGVRGFVPASMVAERFVSDLNQFKNKDIKAQVIEI 121	IVDVNGVRGFVPASN	<i>VDAKVINAVRGGL</i>		HS1

EIB. 36

F16-30

	O)	
319	PS1 173 TK-T -R - TNLT -Y- CEE -V EM -K E IAAV QVDA	PS1
430	-RPG-QVI-EF	RS1
510		ES1
298	HS1 240 SVLEGTVKRVKDFGAFVEILPĠIEGLVHVSQISNKRIENPSEVLKSGDKVQVKVLDIKP	HS1
	·	

299 AEERISLSMKALEEKPERE 317 511 KNRA----VR-KD-AD-KD 529 431 DK -----GI-QL 320 ER -----GV-QLA-DP 335

#S1 PS1 PS1

